

Sequence	Sequence Name(s)	Sequence Description	Ratio	Fold Change	P-value	Sequence ID	Sequence ID
Q0070	AI5_ALPHA	Intron of mitochondrial COX1, a15-alpha; DNA endonuclease involved in intron	2.24	2.24	7.42E-04	SGD	970792
YAL001C	TFC3,FUN24,TSV11	transcription factor tau (TFIIIC) subunit 138; 138 kDa, transcription factor tau (1	0.46	-2.16	8.90E-17	SGD	638922
YAL007C	ERP2	Emp24p/Erv25p related protein 2; p24 protein involved in membrane trafficking	2.93	2.93	6.98E-14	SGD	636524
YAL010C	MDM10,FUN37	Mitochondrial outer membrane protein involved in mitochondrial morphology ar	3.2	3.2	5.44E-05	SGD	638631
YAL014C	YAL014C		2.24	2.24	0	SGD	639165
YAL025C	MAK16	putative nuclear protein; nuclear protein (putative); Null mutant is inviable, conc	2.11	2.11	3.35E-05	SGD	638401
YAL031C	FUN21	Function unknown now; Null mutant is viable	0.37	-2.73	5.12E-14	SGD	636316
YAL034W-	MTW1	Mis TWelve like (a Schizosaccharomyces pombe kinetochore protein); Null mu	2.1	2.1	8.16E-07	SGD	639268
YAL058W	CNE1,FUN48	Functions in endoplasmic reticulum protein quality control; calnexin and calreti	0.45	-2.21	6.41E-14	SGD	638642
YAL060W	BDH1	(2R,3R)-2,3-butanediol dehydrogenase	0.21	-4.86	0	SGD	638512
YAR008W	SEN34,FUN4	tRNA splicing endonuclease 34kDa subunit, homologous to the 42-kDa subuni	2.6	2.6	2.40E-08	SGD	635903
YAR019C	CDC15,LYT1	Required for mitosis and sporulation, cell division cycle blocked at 36 degrees;	0.44	-2.26	1.63E-16	SGD	635581
YAR044W	OSH1	May be involved in ergosterol synthesis; Null mutant is viable but displays pleic	0.39	-2.56	1.01E-17	SGD	635490
YAR053W	YAR053W	predicted membrane protein	2.95	2.95	2.67E-32	SGD	634207
YBL015W	ACH1	Mannose-containing glycoprotein which binds concanavalin A; acetyl CoA hydr	0.37	-2.74	0	SGD	636855
YBL022C	PIM1,LON1	mitochondrial ATP-dependent protease; ATP-dependent protease; no growth c	2.35	2.35	2.22E-27	SGD	633494
YBL023C	MCM2	Member of complex that acts at ARS's to initiate replication; Null mutant is invi	8.14	8.14	1.02E-08	SGD	637300
YBL035C	POL12	Required for DNA synthesis and correct progression through S phase, plays ar	4.45	4.45	0	SGD	634706
YBL041W	PRE7	proteasome subunit; Null mutant is inviable	2.14	2.14	1.08E-43	SGD	633798
YBL042C	FUI1	uridine permease; Null mutant is viable, resistant to 5-fluorouridine and does n	2.73	2.73	5.12E-15	SGD	637143
YBL053W	YBL053W		2.02	2.02	2.03E-15	SGD	637491
YBL077W	YBL077W		2.3	2.3	1.37E-14	SGD	634945
YBL099W	ATP1	mitochondrial F1F0-ATPase alpha subunit; F1F0-ATPase alpha subunit; null r	0.37	-2.67	0	SGD	634023
YBL105C	PKC1,CLY15,HPO2,	Protein Kinase C; The null mutant is inviable and lyses rapidly in hypotonic me	0.39	-2.59	3.38E-16	SGD	637403
YBR018C	GAL7	galactose-1-phosphate uridyl transferase; Null mutant is viable and cannot utili.	3.16	3.16	2.29E-13	SGD	633963
YBR029C	CDS1,CDG1	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidyltransferase, CDP	2.23	2.23	2.48E-11	SGD	633973
YBR042C	YBR042C	Probable membrane-bound small GTPase	2.53	2.53	0	SGD	638502
YBR049C	REB1,GRF2	DNA binding protein which binds sites found in genes transcribed by both RNA	2.1	2.1	4.92E-14	SGD	638126
YBR053C	YBR053C		0.38	-2.62	0	SGD	633883
YBR068C	BAP2	contains 12 predicted transmembrane domains; amino acid permease for leuci	0.45	-2.2	8.20E-34	SGD	636883
YBR070C	YBR070C	involved in osmotolerance	2.07	2.07	1.45E-17	SGD	636630
YBR094W	YBR094W		0.43	-2.3	4.50E-06	SGD	638083
YBR105C	VID24	also involved in vacuolar protein targeting; peripheral vesicle membrane protei	0.48	-2.07	2.95E-36	SGD	633912
YBR116C	YBR116C		0.26	-3.86	2.00E-13	SGD	637571
YBR117C	TKL2	transketolase, homologous to tk11; transketolase, similar to TKL1; Null mutant i	0.44	-2.26	9.90E-09	SGD	638733
YBR148W	YSW1	Spore-specific protein	3.02	3.02	0	SGD	636923

YBR149W	ARA1	D-arabinose dehydrogenase; Null mutant is viable but cannot produce D-arabin	0.5	-2.01	9.12E-16	SGD	637729
YBR166C	TYR1	Step of tyrosine biosynthesis pathway; prephenate dehydrogenase (NADP+); t	2.09	2.09	4.27E-08	SGD	634043
YBR167C	POP7, RPP2	Processing of Precursors; RNase MRP subunit (putative), RNase P integral su	2.92	2.92	1.96E-23	SGD	634346
YBR172C	SMY2	partial suppressor of myo2-66; Null mutant is viable'	2.44	2.44	6.74E-34	SGD	638074
YBR183W	YPC1	Yeast Phyto-ceramidase; alkaline ceramidase with reverse activity; Null mutan	0.43	-2.32	4.55E-24	SGD	636637
YBR196C	PGI1, CDC30	Phosphoglucosomerase; glucose-6-phosphate isomerase; phosphoglucose is	0.24	-4.11	0	SGD	634058
YBR203W	YBR203W		0.29	-3.4	3.02E-25	SGD	638853
YBR206W	YBR206W		0.47	-2.12	1.28E-19	SGD	638137
YBR221C	PDB1	beta subunit of pyruvate dehydrogenase (E1 beta); pyruvate dehydrogenase b	0.48	-2.09	1.72E-16	SGD	636041
YBR222C	FAT2	Fatty acid transporter, very similar to FAT1	0.44	-2.28	2.77E-12	SGD	634080
YBR235W	YBR235W		0.34	-2.98	3.12E-27	SGD	637352
YBR243C	ALG7, TUR1	ER protein that transfers Glc-Nac-P from UDP-GlcNac to Dol-P; UDP-N-acetyl-	2.49	2.49	3.18E-43	SGD	637875
YBR250W	YBR250W		9.16	9.16	0	SGD	635338
YBR270C	YBR270C	Probable ATP/GTP-binding protein	0.41	-2.42	1.43E-29	SGD	636203
YBR274W	CHK1	checkpoint kinase 1, homolog of the S. pombe and mammalian Chk1 checkpoi	0.45	-2.23	9.71E-08	SGD	636873
YBR287W	YBR287W		0.39	-2.54	1.02E-17	SGD	636770
YCL027W	FUS1	cell-surface protein required for cell fusion; Null mutant is viable, in fus1 x fus1	2.08	2.08	4.53E-06	SGD	635344
YCL037C	SRO9	Associates with translating ribosomes, may function in the cytoplasm to modul	2.09	2.09	2.23E-11	SGD	636087
YCL049C	YCL049C		0.39	-2.56	1.33E-38	SGD	636970
YCR011C	ADP1	Shows homology to ATP-dependent permeases	0.45	-2.23	3.13E-16	SGD	634685
YCR019W	MAK32	Protein necessary for structural stability of L-A double-stranded RNA-containin	3.99	3.99	1.98E-16	SGD	639330
YCR020W	HTL1	High-Temperature Lethal; Null mutant is viable but shows temperature-sensitiv	2.98	2.98	2.21E-14	SGD	970797
YCR032W	BPH1	beige protein homologue 1; Null mutant is viable, sensitive to low pH	0.28	-3.54	0	SGD	633515
YCR036W	RBK1	ribokinase	0.47	-2.12	6.11E-30	SGD	633806
YCR102W	ORF:YCR102W-A	BioProcess=biological_process unknown MolFunction=molecular_function unk	2.37	2.37	0	SGD	970817
YDL020C	RPN4, SON1, UFD5	involved in ubiquitin degradation pathway; Null mutant is viable, exhibits synthe	4.18	4.18	6.06E-23	SGD	636905
YDL022W	GPD1, DAR1, HOR1,	glycerol-3-phosphate dehydrogenase; lethal under conditions of osmotic stress	0.37	-2.7	0	SGD	638523
YDL024C	DIA3	involved in invasive and pseudohyphal growth; Null mutant is viable and cause	0.37	-2.73	1.07E-12	SGD	636101
YDL039C	PRM7	pheromone-regulated membrane protein	2.39	2.39	5.46E-16	SGD	637440
YDL040C	NAT1, AAA1	Required for entry into stationary phase, heat shock-resistance, a mating-type	0.49	-2.05	3.85E-06	SGD	637287
YDL048C	STP4	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids	0.3	-3.32	4.19E-23	SGD	637131
YDL064W	UBC9	ubiquitin-conjugating enzyme; Null mutant is inviable	3.2	3.2	0	SGD	637637
YDL098C	SNU23	23 kD U4/U6.U5 snRNP associated protein; RNA binding zinc finger protein (p	2.92	2.92	2.98E-17	SGD	639106
YDL110C	YDL110C		0.25	-3.95	0	SGD	638283
YDL125C	HNT1	Hint homolog, member of the histidine triad superfamily of nucleotide-binding p	0.48	-2.06	2.69E-39	SGD	639176
YDL167C	NRP1	asparagine-rich protein	2.34	2.34	6.45E-22	SGD	638049
YDL215C	GDH2	NAD-dependent glutamate dehydrogenase; Null mutant is viable, grows very p	0.47	-2.13	0	SGD	638891

YDL223C	YDL223C		0.48	-2.1	5.81E-29	SGD	637360
YDL227C	HO	Homothallic switching; homothallic switching endonuclease; Null mutant is viable	2.04	2.04	7.82E-06	SGD	634102
YDL231C	BRE4	contains several putative trans-membrane domains; null mutant is sensitive to	0.48	-2.07	1.51E-24	SGD	633495
YDR028C	REG1,HEX2,PZF24	The reg1 locus encodes a gene which is involved in RNA processing and is a r	0.35	-2.85	1.50E-21	SGD	638833
YDR043C	NRG1	involved in regulation of glucose repression; binds to UAS-1 in the STA1 prom	0.29	-3.5	3.86E-16	SGD	636562
YDR070C	YDR070C		0.34	-2.9	1.40E-37	SGD	634217
YDR089W	YDR089W		0.43	-2.31	2.39E-10	SGD	635504
YDR131C	YDR131C		2.91	2.91	2.36E-11	SGD	636213
YDR178W	SDH4,ACN18	succinate dehydrogenase membrane anchor subunit; Null mutant is viable, ret	0.32	-3.1	4.20E-15	SGD	637551
YDR189W	SLY1	Hydrophilic suppressor of ypt1 involved in vesicle trafficking between ER and C	2.16	2.16	1.37E-23	SGD	637250
YDR194C	MSS116	Mitochondrial RNA helicase of the DEAD box family; RNA helicase DEAD box;	2.4	2.4	0	SGD	635479
YDR204W	COQ4	Involved in ubiquinone biosynthesis; Unable to produce ubiquinone, hypersens	0.44	-2.28	7.22E-31	SGD	637752
YDR213W	UPC2,MOX4	involved in sterol uptake; zinc finger transcription factor of the Zn(2)-Cys(6) bin	2.39	2.39	3.10E-11	SGD	638813
YDR224C	HTB1,SPT12	Histone H2B (HTB1 and HTB2 code for nearly identical proteins); histone H2B	0.36	-2.81	3.53E-08	SGD	633622
YDR232W	HEM1	First enzyme in heme biosynthetic pathway; 5-aminolevulinat synthase; Null r	0.36	-2.79	0	SGD	637975
YDR278C	YDR278C		2.03	2.03	7.73E-10	SGD	638141
YDR293C	SSD1,CLA1,MCS1,F	Product of gene unknown; Suppressor of regulatory subunit of protein kinase	0.49	-2.04	1.66E-06	SGD	638919
YDR388W	RVS167	Involved in endocytosis; cytoskeletal protein (putative); Null mutant is viable bu	0.43	-2.32	5.84E-29	SGD	637103
YDR392W	SPT3	Transcription factor; histone acetyltransferase SAGA complex member, transcr	0.35	-2.82	3.66E-11	SGD	633866
YDR394W	RPT3,YNT1,YTA2	probable 26S protease subunit and member of the CDC48/PAS1/SEC18 family	2.37	2.37	1.17E-27	SGD	637810
YDR399W	HPT1,BRA6	enzyme involved in de novo purine biosynthesis; hypoxanthine guanine phosph	0.29	-3.5	6.66E-14	SGD	636585
YDR436W	PPZ2	serine-threonine phosphatase Z; Null mutant is viable but shows increase in ce	0.46	-2.15	4.33E-24	SGD	636277
YDR457W	TOM1	Temperature dependent Organization in Mitotic nucleus; hect-domain-containir	0.35	-2.84	6.67E-26	SGD	635626
YDR466W	YDR466W		0.47	-2.14	4.32E-38	SGD	634665
YDR483W	KRE2,MNT1	N-glycosylation; alpha-1,2-mannosyltransferase; have altered N-linked glycosy	0.47	-2.12	1.15E-25	SGD	637879
YDR515W	SLF1,SRO99	Associates with translating ribosomes, may function in cytoplasm to modulate r	2.79	2.79	1.92E-28	SGD	633996
YDR517W	GRH1	Yeast (GR)ASP65 (H)omologue; mammalian GRASP protein homolog; Null m	0.3	-3.31	0	SGD	633959
YEL024W	RIP1	oxidizes ubiquinol at center P in the protonmotive Q cycle mechanism, transfer	0.49	-2.04	3.56E-43	SGD	634389
YEL052W	AFG1	ATPase family gene; ATPase family	2.16	2.16	6.11E-33	SGD	636849
YEL060C	PRB1,CVT1	dispensable for haploidization and sporulation, but needed for full protein degr	0.41	-2.46	0	SGD	638721
YER006W	NUG1	NUclear GTPase; Nuclear GTPase involved in Ribosome biogenesis; Null: dea	2.29	2.29	0	SGD	635324
YER012W	PRE1	Required for mitotic division and sporulation; 22.6 kDa proteasome subunit; Nu	2.41	2.41	0	SGD	637616
YER015W	FAA2,FAM1	acyl-CoA synthetase (long-chain fatty acid CoA ligase) (fatty acid activator 2), ;	0.38	-2.66	1.14E-08	SGD	634133
YER033C	ZRG8	Zinc regulated gene	0.44	-2.26	7.68E-28	SGD	638893
YER042W	MXR1,MSRA	peptide Methionine sulfoXide Reductase 1; peptide methionine sulfoxide reduc	2.46	2.46	4.13E-41	SGD	633593
YER047C	SAP1	interacts with Sin1p; AAA ATPase	0.42	-2.36	1.11E-24	SGD	635515
YER054C	GIP2	Glc7-interacting protein, shares homology with PIG2, contains conserved 25 re	2.68	2.68	0	SGD	637921

YER061C	CEM1	homology with beta-keto-acyl synthases; beta-keto-acyl synthase homolog; Nu	0.37	-2.67	7.67E-09	SGD	637816
YER062C	HOR2,GPP2	RHR2 (GPP1) encodes another DL-glycerol-3-phosphatase; DL-glycerol-3-ph	0.44	-2.28	1.71E-36	SGD	639138
YER080W	YER080W		0.43	-2.35	2.11E-10	SGD	635428
YER093C-	YER093C-A		3.99	3.99	9.54E-22	SGD	633386
YER119C	YER119C	similar to amino acid transport proteins	0.44	-2.28	4.24E-17	SGD	637812
YER125W	RSP5,MDP1,MUT2,I	involved in ubiquitin-mediated protein degradation; Null mutant is inviable, an r	0.45	-2.21	1.43E-07	SGD	638111
YER143W	DDI1,VSM1	DNA Damage Inducible, binds to T- and V- snare complexes; Null mutant is via	2.53	2.53	2.78E-37	SGD	637826
YER155C	BEM2,IPL2,SUP9,T	Protein with role in bud emergence; rho GTPase activating protein (GAP); rand	0.43	-2.31	1.95E-17	SGD	633531
YER164W	CHD1	Sole <i>S. cerevesiae</i> member of CHD gene family containing Chromodomain, He	0.43	-2.3	8.99E-07	SGD	635637
YER166W	DNF1	Drs2 Neo1 Family; Potential aminophospholipid translocase; viable	0.38	-2.63	0	SGD	633581
YER178W	PDA1	alpha subunit of pyruvate dehydrogenase (E1 alpha); pyruvate dehydrogenase	0.49	-2.05	1.16E-21	SGD	633945
YER185W	YER185W		3.84	3.84	4.90E-14	SGD	634549
YFL034C-/	RPL22B	Homology to rat L22; ribosomal protein L22B (L1c) (rp4) (YL31)	2.28	2.28	1.69E-06	SGD	970761
YFR003C	YFR003C		2.27	2.27	9.42E-36	SGD	634999
YFR004W	RPN11,MPR1	Suppressor of mutant (ts on glycerol) tRNA gene deficient in the processing of	2.87	2.87	0	SGD	635144
YFR010W	UBP6	deubiquitinating enzyme (putative)	2.78	2.78	4.80E-18	SGD	636871
YFR022W	YFR022W		0.31	-3.24	4.23E-20	SGD	636222
YFR043C	YFR043C		2.39	2.39	5.83E-07	SGD	635095
YFR050C	PRE4	B-type subunit of proteasome, euk. & archae. multicatalytic proteinase comple	2.95	2.95	8.31E-43	SGD	633713
YGL009C	LEU1	leucine biosynthesis; isopropylmalate isomerase; Leucine requiring	0.42	-2.4	5.83E-38	SGD	634182
YGL015C	YGL015C		4.39	4.39	1.99E-31	SGD	635725
YGL029W	CGR1	coiled-coil growth-regulated; coiled-coil protein; Null mutant is inviable, CGR1 €	3.9	3.9	1.47E-40	SGD	635658
YGL035C	MIG1,CAT4,SSN1,T	Transcription factor involved in glucose repression; C2H2 zinc finger protein th	0.33	-3	0	SGD	637132
YGL057C	YGL057C		2.22	2.22	7.43E-12	SGD	637694
YGL078C	DBP3	ATP-dependent RNA helicase CA3 of the DEAD/DEAH box family; ATP depen	2.05	2.05	7.45E-18	SGD	638672
YGL122C	NAB2	nuclear polyadenylated RNA binding protein; polyadenylated RNA binding prot	2.21	2.21	9.54E-16	SGD	636856
YGL140C	YGL140C		0.47	-2.13	3.11E-11	SGD	637346
YGL148W	ARO2	Chorismate synthase; chorismate synthase; aromatic amino acid requiring, lac	2.31	2.31	2.03E-40	SGD	638516
YGL156W	AMS1	vacuolar alpha mannosidase; alpha mannosidase; null mutant is viable	0.37	-2.71	0	SGD	633499
YGL173C	KEM1,DST2,RAR5,ξ	Kar1-1 nuclear-fusion-defect Enhancing Mutation. Plays a role in cytoplasmic r	0.39	-2.59	1.43E-09	SGD	638901
YGL188C	YGL188C		2.57	2.57	1.45E-08	SGD	634790
YGL214W	YGL214W		2.37	2.37	1.39E-20	SGD	636535
YGL217C	YGL217C		2.29	2.29	1.81E-25	SGD	639026
YGL224C	SDT1,SSM1	suppressor of deletion of TFIS; null mutant is viable, but is sensitive to 6-azau	2.04	2.04	2.09E-12	SGD	637715
YGL227W	VID30	vacuole import and degradation (VID), TOR inhibitor (TIN); Null mutant is viabl	0.35	-2.89	9.17E-06	SGD	637371
YGR032W	GSC2,FKS2	Highly similar to FKS1 (GSC1). GSC2 and FKS1 encode redundant catalytic c	0.35	-2.86	9.32E-21	SGD	638911
YGR043C	YGR043C		0.38	-2.65	1.11E-07	SGD	635908

YGR048W	UFD1	Ubiquitin fusion degradation protein; Homozygous ufd1-1 mutant diploids exhibit	3.66	3.66	0	SGD	637838
YGR070W	ROM1,SKC1	Gdp-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein; N	0.41	-2.46	5.11E-42	SGD	637387
YGR127W	YGR127W		0.39	-2.58	1.12E-17	SGD	638442
YGR143W	SKN1	Involved in (1->6)-beta-glucan biosynthesis; highly homologous to Kre6p, type	2.81	2.81	2.57E-17	SGD	638077
YGR170W	PSD2	converts phosphatidylserine to phosphatidylethanolamine; phosphatidylserine	0.43	-2.33	5.60E-11	SGD	638887
YGR201C	YGR201C		0.37	-2.71	3.52E-07	SGD	633767
YGR214W	RPS0A,NAB1,NAB1	Homology to rat Sa; ribosomal protein S0A; Null mutant is viable, yst1 (rps0a)	3.75	3.75	0	SGD	637047
YGR215W	RSM27	mitochondrial ribosome small subunit component	2.22	2.22	1.55E-05	SGD	636407
YGR234W	YHB1,YHB4	may play a role in the oxidative stress response; flavohemoglobin; Null mutant	3.05	3.05	0	SGD	635207
YGR240C	PFK1	phosphofructokinase alpha subunit; Null mutant is viable, accumulates fructose	0.34	-2.98	0	SGD	637319
YGR243W	YGR243W		0.3	-3.32	0	SGD	638207
YGR248W	SOL4	similar to SOL3	0.35	-2.82	4.71E-25	SGD	634500
YGR249W	MGA1	Mga1p shows similarity to heat shock transcription factor; similar to heat shock	2.51	2.51	1.91E-23	SGD	634040
YGR263C	YGR263C		2.02	2.02	1.29E-14	SGD	637051
YGR265W	YGR265W		2.99	2.99	1.15E-10	SGD	634936
YGR266W	YGR266W		0.49	-2.05	0	SGD	638054
YGR270W	YTA7	Member of CDC48/PAS1/SEC18 family of ATPases	0.42	-2.41	2.68E-08	SGD	637413
YGR287C	YGR287C		0.41	-2.46	1.98E-16	SGD	634731
YGR289C	MAL11,AGT1	Part of MAL1 complex locus, encodes funct. maltose permease in all strains, e	0.34	-2.92	1.73E-13	SGD	637205
YHL005C	YHL005C		2.15	2.15	2.70E-19	SGD	638984
YHL019C	APM2	homologous to the medium chain of mammalian clathrin-associated protein coi	0.43	-2.33	1.10E-10	SGD	637194
YHL029C	YHL029C		2.65	2.65	2.96E-34	SGD	635458
YHL047C	TAF1,ARN2	Siderophore transporter for triacetylfusarinine C; triacetylfusarinine C transport	0.48	-2.08	2.68E-39	SGD	637186
YHR001W	QCR10	8.5 kDa subunit of the ubiquinol-cytochrome c oxidoreductase complex; ubiquin	0.43	-2.32	7.09E-07	SGD	633421
YHR042W	NCP1,CPR1	NADP-cytochrome P450 reductase; Null mutant is viable	0.47	-2.15	8.16E-05	SGD	634569
YHR062C	RPP1	Ribonuclease P protein 1, required for processing of precursor tRNA and 35S p	2.9	2.9	2.82E-07	SGD	633808
YHR065C	RRP3	Required for maturation of the 35S primary transcript of pre-rRNA and is requir	2.46	2.46	9.01E-22	SGD	636144
YHR077C	NMD2,IFS1,SUA1,U	Protein involved in decay of mRNA containing nonsense codons; Null mutant is	0.49	-2.05	4.86E-13	SGD	633435
YHR078W	YHR078W		0.42	-2.38	0	SGD	634019
YHR096C	HXT5	Member of superfamily of monosaccharide transporters; hexose transporter; N	0.29	-3.42	1.94E-37	SGD	634730
YHR102W	KIC1,NRK1	Kinase that interacts with Cdc31p, N-rich kinase 1	0.34	-2.94	6.11E-21	SGD	633436
YHR108W	GGA2	Golgi-localized, gamma-adaptin homology, Arf-binding; ARF-binding protein	2.03	2.03	7.95E-21	SGD	636241
YHR135C	YCK1,CKI2	membrane-bound casein kinase I homolog; casein kinase I homolog; Null muta	0.43	-2.31	1.93E-05	SGD	636147
YIL047C	SYG1	Protein for which truncation and overexpression can suppress lethality of G-alf	0.33	-3	0	SGD	635498
YIL075C	RPN2,SEN3	involved in tRNA processing and degradation of ubiquitinated proteins; Null mu	2.39	2.39	4.54E-08	SGD	634678
YIL078W	THS1	Threonyl-tRNA synthetase, cytoplasmic; threonine-tRNA ligase	2.1	2.1	6.67E-29	SGD	638030
YIL097W	FYV10	Function required for Yeast Viability on toxin exposure; Null mutant is viable bu	0.35	-2.84	1.06E-07	SGD	638618

YIL125W	KGD1,OGD1	alpha-ketoglutarate dehydrogenase; Null mutant is viable but is deficient in alpl	0.46	-2.19	9.42E-12	SGD	637309
YIL155C	GUT2	glycerol-3-phosphate dehydrogenase, mitochondrial; glycerol-3-phosphate deh	0.37	-2.71	8.45E-10	SGD	638727
YIR007W	YIR007W		0.39	-2.54	6.45E-13	SGD	634805
YIR020W	ORF:YIR020W-B	BioProcess=biological_process unknown MolFunction=molecular_function unk	2.01	2.01	4.22E-31	SGD	970760
YJL005W	CYR1,CDC35,HSR1	Required for START A of cell cycle, and glucose and nitrogen repression of sp	0.39	-2.55	3.13E-14	SGD	633592
YJL016W	YJL016W		0.35	-2.87	0	SGD	639057
YJL028W	YJL028W		2.12	2.12	6.75E-30	SGD	637447
YJL060W	YJL060W		2.44	2.44	0	SGD	633998
YJL082W	IML2	Similar to Ykr018p	0.38	-2.66	2.23E-28	SGD	634194
YJL084C	YJL084C		0.31	-3.24	1.99E-12	SGD	634701
YJL132W	YJL132W		0.41	-2.44	6.07E-33	SGD	638084
YJL134W	LCB3,LBP1,YSR2	Protein involved in incorporation of exogenous long chain bases in sphingolipic	0.35	-2.85	7.78E-20	SGD	638564
YJL186W	MNN5	mannan synthesis; golgi alpha-1,2-mannosyltransferase (putative); Null mutant	0.27	-3.73	0	SGD	636240
YJL218W	YJL218W		2.34	2.34	5.21E-22	SGD	637619
YJL220W	YJL220W		4.4	4.4	5.13E-15	SGD	634320
YJR024C	YJR024C		2.58	2.58	3.24E-31	SGD	637650
YJR030C	YJR030C		2.44	2.44	1.23E-14	SGD	634191
YJR033C	RAV1	Regulator of (H+)-ATPase in vacuolar membrane	0.3	-3.32	1.02E-21	SGD	633528
YJR073C	OPI3,PEM2	Second and third steps of methylation pathway for phosphatidylcholine biosynt	0.34	-2.96	0	SGD	639181
YJR091C	JSN1,PUF1	benomyl dependent tubulin mutant; Overexpression suppresses some tub2 all	2.29	2.29	7.14E-19	SGD	635599
YJR121W	ATP2	F(1)F(0)-ATPase complex beta subunit, mitochondrial; F(1)F(0)-ATPase comp	0.4	-2.48	1.81E-24	SGD	638663
YJR127C	ZMS1	Product of gene unknown	0.47	-2.11	2.61E-04	SGD	637471
YJR151C	DAN4	Delayed Anaerobic Gene; cell wall mannoprotein; unknown	0.35	-2.86	1.71E-24	SGD	638924
YJR155W	AAD10	high degree of similarity with the AAD of P. chrysosporium; aryl-alcohol dehydr	0.46	-2.18	3.94E-12	SGD	637760
YKL010C	UFD4	Ubiquitin Fusion Degradation; Null is viable, defective in proteolysis of fusion p	0.38	-2.6	0	SGD	638949
YKL015W	PUT3	Positive regulator of PUT (proline utilization) genes; zinc finger transcription fac	4.4	4.4	3.48E-26	SGD	634698
YKL020C	SPT23	Dosage dependent suppressor of Ty-induced promoter mutations; Null mutant	0.45	-2.24	1.16E-08	SGD	635600
YKL038W	RGT1	transcriptional repressor and activator; transcriptional activator, transcriptional	0.34	-2.98	0	SGD	637402
YKL054C	VID31	Vacuole import and degradation	2.76	2.76	2.98E-14	SGD	636221
YKL055C	OAR1	3-oxoacyl-[acyl-carrier-protein] reductase; Null mutant is viable, respiratory def	2.34	2.34	7.51E-12	SGD	635938
YKL060C	FBA1	aldolase; Null mutant is viable, lacks aldolase enzymatic activity and fails to grc	0.41	-2.44	6.69E-24	SGD	639349
YKL076C	YKL076C		0.44	-2.3	1.94E-07	SGD	637488
YKL082C	YKL082C		2.89	2.89	0	SGD	634005
YKL083W	YKL083W		2.52	2.52	5.02E-18	SGD	633286
YKL093W	MBR1	Involved in mitochondrial biogenesis; Null mutant is viable, shows defective grc	2.29	2.29	2.63E-16	SGD	633802
YKL100C	YKL100C		0.38	-2.62	6.73E-20	SGD	634117
YKL106W	AAT1	aspartate aminotransferase, mitochondrial; aspartate aminotransferase; Null m	2.45	2.45	2.53E-17	SGD	639355

YKL114C	APN1	major apurinic/apurimidinic endonuclease/3'-repair diesterase; hypersensitive t	2.12	2.12	1.31E-20	SGD	636009
YKL115C	YKL115C		2.81	2.81	0	SGD	639000
YKL116C	PRR1	protein kinase	2.3	2.3	2.45E-07	SGD	638617
YKL151C	YKL151C		0.32	-3.15	2.80E-45	SGD	639298
YKL174C	YKL174C	probable transport protein	0.41	-2.44	2.88E-11	SGD	637189
YKL176C	LST4	involved in regulated secretion/recycling of nitrogen regulated permeases; very	0.5	-2.01	3.65E-12	SGD	634808
YKL205W	LOS1	Nuclear pore protein involved in pre-tRNA splicing; Null mutant is viable but is i	2.58	2.58	0	SGD	638890
YKL220C	FRE2	Ferric reductase, similar to Fre1p; ferric reductase	0.35	-2.84	2.06E-19	SGD	638051
YKR028W	SAP190	190 kDa protein that associates with the SIT4 phosphatase in a cell cycle depe	0.45	-2.22	5.58E-07	SGD	637354
YKR096W	YKR096W		0.41	-2.47	4.38E-34	SGD	635607
YLL015W	BPT1	bile pigment transporter; ABC transporter, highly homologous to human MRP1	0.3	-3.36	1.34E-28	SGD	635691
YLL032C	YLL032C		0.44	-2.27	1.74E-23	SGD	634824
YLL040C	VPS13,SOI1,VPT2	vacuolar Protein Sorting; Null mutant is viable but exhibits defects in vacuolar p	0.34	-2.91	4.41E-12	SGD	638954
YLL046C	RNP1	ribonucleoprotein 1; RNA binding protein (putative); Null mutant is viable	2.36	2.36	1.86E-18	SGD	635885
YLR020C	YLR020C		2.44	2.44	1.72E-10	SGD	639484
YLR038C	COX12	essential during assembly for full cytochrome c oxidase activity; cytochrome c i	0.47	-2.13	0	SGD	638197
YLR046C	YLR046C		0.44	-2.26	3.42E-08	SGD	633771
YLR066W	SPC3	signal peptidase subunit; Null mutant is inviable.	2.65	2.65	6.42E-07	SGD	637549
YLR067C	PET309	Involved in expression of mitochondrial COX1 by regulating translation of COX	2.44	2.44	3.72E-35	SGD	638809
YLR075W	RPL10,GRC5,QSR1	similar to members of the QM gene family, which is implicated in differentiation	2.7	2.7	3.44E-13	SGD	638296
YLR076C	YLR076C		3.57	3.57	1.47E-29	SGD	634253
YLR120C	YPS1	Gpi-anchored aspartic protease (Yapsin 1); GPI-anchored aspartic protease; N	0.38	-2.64	0	SGD	638000
YLR149C	YLR149C		0.3	-3.35	2.95E-23	SGD	634779
YLR178C	TFS1,DKA1	(putative) lipid binding protein, supressor of a cdc25 mutation; lipid binding prot	0.49	-2.02	5.27E-25	SGD	636587
YLR179C	YLR179C		0.46	-2.19	1.02E-11	SGD	637598
YLR180W	SAM1,ETH10	S-adenosylmethionine synthetase; Null mutant is viable.	0.42	-2.37	2.25E-06	SGD	635234
YLR189C	UGT51	Udp-glycosyltransferase; UDP-glucose:sterol glucosyltransferase; Null mutant	0.43	-2.31	1.29E-33	SGD	633490
YLR212C	TUB4	spindle pole body component that organizes both cytoplasmic and nuclear mic	2.11	2.11	3.61E-10	SGD	637893
YLR214W	FRE1	Ferric (and cupric) reductase; cupric reductase, ferric reductase; Null mutant is	2.55	2.55	3.62E-15	SGD	638732
YLR217W	YLR217W		3.58	3.58	3.92E-44	SGD	634834
YLR241W	YLR241W		0.43	-2.33	5.47E-42	SGD	634232
YLR294C	YLR294C		0.49	-2.03	2.48E-05	SGD	636426
YLR305C	STT4,BLM1	functions in the PKC1 protein kinase pathway, in a pathway with STT1 and MS	0.49	-2.05	1.10E-26	SGD	638974
YLR348C	DIC1	mitochondrial dicarboxylate transport protein; dicarboxylate transport protein	0.21	-4.87	2.06E-28	SGD	635065
YLR352W	YLR352W		0.45	-2.22	2.10E-18	SGD	634746
YLR356W	YLR356W		0.43	-2.34	0	SGD	633735
YLR368W	YLR368W		0.44	-2.27	0	SGD	634113

YLR371W	ROM2	Gdp-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein, I	0.46	-2.17	3.23E-10	SGD	635625
YLR372W	SUR4,ELO3,SRE1, V	Required for conversion of 24-carbon fatty acids to 26-carbon species; Null mu	2.42	2.42	0	SGD	633875
YLR425W	TUS1,SOP10	TOR Unique function Suppressor, exchange factor for RHO1; 1307 amino acid	0.42	-2.4	0	SGD	637380
YLR452C	SST2	Protein involved in desensitization to alpha-factor pheromone; GTPase activati	0.33	-3.01	8.13E-37	SGD	636282
YLR454W	YLR454W		0.43	-2.34	1.13E-17	SGD	635699
YLR457C	NBP1	Nap1p Binding Protein; Null mutant is inviable	2.98	2.98	2.09E-16	SGD	634518
YLR458W	YLR458W		2.37	2.37	1.30E-30	SGD	633629
YML009C-	ORF:YML009C-A	BioProcess=biological_process unknown MolFunction=molecular_function unk	2.17	2.17	9.69E-19	SGD	970811
YML032C	RAD52	Required for X-ray damage repair & various types of intra- and interchr. mitotic	2.88	2.88	7.74E-20	SGD	636868
YML035C	AMD1,AMD3	putative alpha-mannosidase; alpha-mannosidase (putative); Null mutant is viat	0.42	-2.36	0	SGD	636371
YML043C	RRN11	rDNA transcription factor CF component, which also contains Rrn6p and Rrn7p	2.28	2.28	4.19E-28	SGD	637130
YML046W	PRP39	May function to facilitate or stabilize the interaction between U1 snRNP and the	2.23	2.23	0	SGD	638703
YML047W-	ORF:YML047W-A	BioProcess=biological_process unknown MolFunction=molecular_function unk	3.26	3.26	2.06E-15	SGD	970725
YML059C	YML059C		0.31	-3.26	1.01E-26	SGD	633520
YML092C	PRE8	proteasome component Y7	3.13	3.13	4.58E-38	SGD	637677
YML093W	YML093W		2.74	2.74	6.98E-36	SGD	637279
YML100W	TSL1	123 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase cor	0.42	-2.37	2.66E-05	SGD	637392
YML102W	CAC2	Involved in DNA-replication-linked nucleosome assembly, homologous to the p	0.45	-2.23	3.61E-05	SGD	639404
YML110C	COQ5,DBI56	co-enzyme Q deficient; C-methyltransferase (putative); Null mutant is viable, re	0.28	-3.55	0	SGD	636609
YML116W-	ORF:YML116W-A	BioProcess=biological_process unknown MolFunction=molecular_function unk	0.35	-2.83	1.50E-20	SGD	970714
YML117W	YML117W		0.4	-2.51	8.99E-12	SGD	637351
YML128C	MSC1	Meiotic Sister-Chromatid recombination	0.47	-2.14	0	SGD	637127
YMR004W	MVP1	Protein required for sorting proteins to the vacuole; MVP1 was identified as a n	2.68	2.68	2.39E-09	SGD	637128
YMR007W	YMR007W		0.47	-2.15	8.73E-11	SGD	635715
YMR020W	FMS1	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows simila	0.48	-2.08	1.22E-09	SGD	638680
YMR029C	YMR029C		0.45	-2.23	1.18E-28	SGD	638615
YMR067C	YMR067C		3.48	3.48	1.02E-29	SGD	638607
YMR083W	ADH3	alcohol dehydrogenase isoenzyme III; Null mutant is viable	0.26	-3.8	0	SGD	636035
YMR119W	YMR119W-A		0.29	-3.5	4.55E-08	SGD	637492
YMR129W	POM152	May be involved in duplication of nuclear pores and nuclear pore complexes du	0.4	-2.48	0	SGD	635585
YMR145C	YMR145C		0.28	-3.63	3.99E-31	SGD	636212
YMR153W	NUP53	Component of karyopherin docking complex of the nuclear pore complex; karyo	0.45	-2.23	0	SGD	634029
YMR162C	DNF3	Drs2 Neo1 Family; Potential aminophospholipid translocase; viable	0.45	-2.24	7.55E-19	SGD	637377
YMR169C	ALD3	Expression induced in response to heat shock, oxidative and osmotic stress. N	2.08	2.08	9.88E-13	SGD	633415
YMR172C-	YMR172C-A		2.8	2.8	4.05E-15	SGD	635745
YMR181C	YMR181C		0.34	-2.95	0	SGD	636471
YMR196W	YMR196W		0.38	-2.61	0	SGD	638876

YMR206W	YMR206W		0.36	-2.81	7.19E-05	SGD	636706
YMR218C	TRS130	targeting complex (TRAPP) component involved in ER to Golgi membrane traf	0.47	-2.12	1.44E-10	SGD	633497
YMR219W	ESC1	Establishes Silent Chromatin	0.39	-2.54	3.91E-36	SGD	638961
YMR221C	YMR221C		0.4	-2.49	3.77E-04	SGD	635366
YMR226C	YMR226C		0.47	-2.11	8.03E-15	SGD	639151
YMR232W	FUS2	Involved in cell fusion during mating, also required for the alignment of parenta	0.32	-3.1	1.85E-20	SGD	638794
YMR237W	YMR237W		0.39	-2.56	3.96E-20	SGD	638090
YMR256C	COX7	subunit VII of cytochrome c oxidase; cytochrome c oxidase subunit VII; Null mu	0.39	-2.57	2.27E-05	SGD	634201
YMR258C	YMR258C		0.49	-2.02	1.14E-09	SGD	637918
YMR276W	DSK2	Required with RAD23 for duplication of the spindle pole body; ubiquitin-like pro	2.32	2.32	1.30E-32	SGD	636021
YMR280C	CAT8,DIL1,MSP8	Zinc-cluster protein involved in activating gluconeogenic genes, related to Gal4	0.4	-2.52	4.44E-34	SGD	635695
YMR297W	PRC1,LBC1	dispensable for haploidization and sporulation, but required for full protein degr	0.32	-3.17	0	SGD	636889
YMR304W	UBP15	putative deubiquitinating enzyme; deubiquitinating enzyme (putative)	0.28	-3.52	1.96E-21	SGD	633488
YMR317W	YMR317W		2.31	2.31	2.57E-37	SGD	638871
YNL015W	PBI2	Proteinase inhibitor that inhibits protease Prb1p (yscB); proteinase inhibitor I2E	0.46	-2.15	3.38E-06	SGD	638188
YNL020C	ARK1	actin regulating kinase; serine/threonine kinase (putative); Null mutant is viable	0.45	-2.25	3.62E-08	SGD	637202
YNL031C	HHT2	Histone H3 (HHT1 and HHT2 code for identical proteins); histone H3 (HHT1 ar	0.35	-2.87	7.91E-13	SGD	634350
YNL032W	SIW14	Synthetic interaction with Whi2; tyrosine phosphatase; Null mutant fails to shov	0.48	-2.08	2.38E-08	SGD	633834
YNL036W	NCE103	involved in secretion of proteins that lack classical secretory signal sequences;	2.42	2.42	0	SGD	634452
YNL037C	IDH1	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1; isocitrate c	0.24	-4.13	5.53E-14	SGD	637768
YNL065W	AQR1	A(acids, azoles) Q(quinidine, quinine) Resistance; multidrug resistance transpc	3.49	3.49	0	SGD	639491
YNL073W	MSK1	mitochondrial lysine-tRNA synthetase; lysine-tRNA ligase; An uncharacterized	2.04	2.04	2.07E-17	SGD	637996
YNL091W	YNL091W		0.4	-2.5	4.74E-38	SGD	635604
YNL097C	PHO23	Involved in expression of PHO5; Null mutant is viable but shows constitutive PI	0.49	-2.05	2.26E-13	SGD	638427
YNL129W	YNL129W		2.53	2.53	0	SGD	633799
YNL138W	SRV2,CAP	70-kDa adenylyl cyclase-associated protein; 70 kDa adenylyl cyclase-associat	0.41	-2.47	1.23E-04	SGD	638655
YNL144C	YNL144C		0.45	-2.23	4.31E-39	SGD	636287
YNL151C	RPC31,ACP2,RPC8	31-kDa subunit of RNA polymerase III (C), HMG1 like protein; HMG1-like prote	2.51	2.51	2.84E-12	SGD	635024
YNL163C	RIA1	Ribosome Assembly; Null: quasi essential. Other phenotypes: Depletion of Ria	0.5	-2.01	5.27E-10	SGD	638928
YNL183C	NPR1	protein kinase homolog; inactive ammonia-sensitive amino acid permeases	2.78	2.78	9.10E-36	SGD	636375
YNL184C	YNL184C		2.22	2.22	9.61E-07	SGD	634265
YNL188W	KAR1	involved in spindle pole body duplication and karyogamy, interacts with Cdc31;	2.73	2.73	1.05E-37	SGD	637852
YNL211C	YNL211C		2.35	2.35	3.37E-11	SGD	634218
YNL218W	MGS1	Maintenance of Genome Stability 1	0.39	-2.54	6.25E-20	SGD	636180
YNL224C	YNL224C		0.49	-2.05	1.43E-19	SGD	634820
YNL268W	LYP1	lysine permease	0.42	-2.4	2.80E-25	SGD	636922
YNL280C	ERG24	sterol C-14 reductase; Null mutant appears to be inviable in some genetic back	0.47	-2.12	0	SGD	633372

YNL295W	YNL295W		0.44	-2.28	2.31E-39	SGD	636841
YNL310C	YNL310C		0.48	-2.09	2.21E-10	SGD	639112
YNL313C	YNL313C		2.05	2.05	1.31E-12	SGD	635482
YNL317W	PFS2	Polyadenylation Factor I subunit 2; polyadenylation factor subunit; Null mutant	0.45	-2.22	0	SGD	639437
YNL321W	YNL321W		0.43	-2.3	0	SGD	638829
YNL329C	PEX6,PAS8	Required for peroxisome assembly; AAA ATPase; lack of peroxisome biogene:	0.35	-2.88	0	SGD	637362
YNR002C	FUN34	Highly homologous to Ycr010p and similar to Yarrowia lipolytica glyoxylate patl	0.41	-2.42	0	SGD	633761
YNR019W	ARE2,SAT1	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase); acyl-CoA chole	3.88	3.88	0	SGD	637179
YNR020C	YNR020C		2.32	2.32	2.11E-07	SGD	639231
YNR024W	YNR024W		2.02	2.02	6.60E-05	SGD	639128
YNR034W	SOL1	Multicopy Suppressor Of los1; Null mutant is viable	2.41	2.41	3.30E-09	SGD	638480
YNR064C	YNR064C		3.27	3.27	1.14E-09	SGD	637708
YNR072W	HXT17	Hexose transporter; hexose transporter	2.37	2.37	5.50E-38	SGD	639470
YOL013C	HRD1,DER3	Ubiquitin-protein ligase for endoplasmic reticulum-associated degradation.; Nu	0.38	-2.64	2.49E-16	SGD	639526
YOL016C	CMK2	Calmodulin-dependent protein kinase; calmodulin-dependent protein kinase; N	0.27	-3.66	4.57E-20	SGD	636117
YOL020W	TAT2,LTG3,SAB2,S	Tryptophan permease, high affinity; tryptophan permease, high affinity; suppre	0.49	-2.05	4.44E-09	SGD	637988
YOL032W	YOL032W		2.25	2.25	8.16E-10	SGD	637664
YOL057W	YOL057W		3.79	3.79	4.62E-21	SGD	634140
YOL068C	HST1	Homolog of SIR2; Overexpression restores transcriptional silencing in a sir2 m	2.51	2.51	8.47E-41	SGD	635314
YOL082W	CVT19	Cytoplasm to Vacuole Targeting, Mutant is defective in import of aminopeptida:	0.42	-2.4	1.53E-14	SGD	635252
YOL084W	PHM7	transcription is regulated by PHO system	0.33	-3.05	1.49E-24	SGD	637311
YOL086C	ADH1,ADC1	Alcohol dehydrogenase; alcohol dehydrogenase; Null mutant is viable and sen	0.41	-2.45	1.23E-23	SGD	633922
YOL087C	YOL087C		0.46	-2.15	6.47E-08	SGD	638873
YOL089C	HAL9	involved in salt tolerance; contains zinc finger, transcription factor (putative); Ni	0.38	-2.65	0	SGD	637308
YOL094C	RFC4	RFC is a DNA binding protein and ATPase that acts as a processivity factor for	2.06	2.06	0	SGD	636977
YOL096C	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; Null mutant is viable, f	0.35	-2.82	2.35E-34	SGD	635190
YOL104C	NDJ1,TAM1	Involved in meiotic chromosome segregation, may stabilize homologous DNA in	2	2	1.16E-08	SGD	633854
YOL122C	SMF1,SBS1	Isolated as high copy suppressor of a cdc1 mutation & involved in high affinity	2.43	2.43	2.22E-10	SGD	637960
YOL130W	ALR1	aluminium resistance; ion transporter (putative); Null mutant is inviable, overex	0.46	-2.17	2.77E-09	SGD	637302
YOL133W	HRT1,RBX1,ROC1	High level expression Reduces Ty3 Transposition; Skp1-Cullin-F-box ubiquitin	0.42	-2.38	4.83E-29	SGD	639014
YOR014W	RTS1	B-type regulatory subunit of protein phosphatase 2A (PP2A); protein phosphat:	0.43	-2.34	5.10E-33	SGD	634757
YOR015W	YOR015W		0.4	-2.53	1.45E-13	SGD	633658
YOR031W	CRS5	Metallothionein-like protein; metallothionein-like protein; Null mutant is viable, ε	0.47	-2.13	1.61E-17	SGD	638198
YOR040W	GLO4	Mitochondrial glyoxylase-II; glyoxylase-II; Null mutant is viable, but shows incre	0.48	-2.07	4.69E-08	SGD	639187
YOR041C	YOR041C		0.46	-2.18	6.78E-05	SGD	634913
YOR065W	CYT1,CTC1	Cytochrome c1; cytochrome c1	0.4	-2.53	9.06E-12	SGD	634483
YOR070C	GYP1	Gtpase activating protein for Ypt1p; GTPase activating protein (GAP); Null mut	0.33	-3.07	7.02E-32	SGD	638690

YOR109W INP53,SJL3,SOP2	Synaptojanin-like protein; inositol polyphosphate 5-phosphatase; Null mutant is	0.39	-2.57	0	SGD	637391
YOR136W IDH2	NAD ⁺ -dependent isocitrate dehydrogenase; NAD-dependent isocitrate dehydr	0.37	-2.72	4.54E-10	SGD	633891
YOR161C YOR161C		0.45	-2.24	2.15E-20	SGD	634026
YOR173W YOR173W		0.33	-3.01	2.36E-17	SGD	638535
YOR178C GAC1	Regulatory subunit for phosphoprotein phosphatase type 1 (PP-1), also known	0.37	-2.74	2.54E-22	SGD	634179
YOR204W DED1,SPP81	ATP-dependent RNA helicase of DEAD box family, suppressor of a pre-mRNA	2.51	2.51	6.68E-05	SGD	636886
YOR266W PNT1	Involved in targeting of proteins to the mitochondrial inner membrane, Pentami	3.18	3.18	9.37E-14	SGD	635248
YOR273C TPO4	Polyamine transport protein	0.43	-2.34	3.97E-34	SGD	638799
YOR285W YOR285W		0.26	-3.79	0	SGD	636385
YOR288C MPD1	Disulfide isomerase related protein; disulfide isomerase related protein; Null m	0.43	-2.35	5.23E-07	SGD	636702
YOR291W YOR291W		0.25	-3.96	1.55E-40	SGD	633584
YOR292C YOR292C		0.45	-2.2	6.80E-23	SGD	635142
YOR298C- MBF1	bridges the DNA-binding region of GCN4 and TBP, similar to multiprotein bridg	0.43	-2.31	2.82E-34	SGD	970752
YOR303W CPA1	Carbamoyl phosphate synthetase, arginine specific; arginine specific, carbamo	0.43	-2.33	3.39E-11	SGD	636795
YOR309C YOR309C		2.76	2.76	1.02E-16	SGD	635731
YOR310C NOP58	57 kDa nucleolar protein involved in the pre-rRNA processing steps that lead to	2.54	2.54	6.73E-19	SGD	636848
YOR325W YOR325W		6.65	6.65	3.79E-37	SGD	634982
YOR329C SCD5,FTB1	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1; Null muta	0.44	-2.25	2.80E-10	SGD	634654
YOR333C YOR333C		2.92	2.92	7.29E-05	SGD	634950
YOR356W YOR356W		0.4	-2.52	8.74E-28	SGD	635369
YOR361C PRT1,CDC63,DNA2	translation initiation factor eIF3 subunit; Null mutant is inviable.	3.06	3.06	2.91E-18	SGD	636264
YOR371C KRH2	Kelch Repeat Homologue. Homologue of KRH1. Does not act in the cAMP-PK.	0.5	-2.01	3.18E-06	SGD	638776
YOR377W ATF1	Alcohol acetyltransferase; alcohol acetyltransferase	0.38	-2.63	1.15E-21	SGD	638614
YPL022W RAD1,LPB9	UV endonuclease; radiation sensitive	0.42	-2.41	8.36E-09	SGD	638929
YPL026C SKS1,SHA3	multicopy suppressor of snf3 and grr1 mutants; Null mutant is viable, Sks1 lack	0.32	-3.09	2.78E-12	SGD	638627
YPL049C DIG1,RST1	Down-regulator of Invasive Growth, Regulator of Sterile Twelve, binds Fus3 an	0.41	-2.42	8.56E-06	SGD	633977
YPL057C SUR1,BCL21,CSG1	Involved in maintenance of phospholipid levels; integral membrane protein, sim	0.32	-3.14	3.17E-09	SGD	638528
YPL084W BRO1,LPF2	BCK1-like resistance to osmotic shock; Temperature-sensitive growth defect, s	0.38	-2.64	1.86E-12	SGD	635493
YPL087W YDC1	Yeast dihydro-ceramidase; alkaline dihydroceramidase with minor reverse acti	0.46	-2.18	6.07E-05	SGD	638438
YPL107W YPL107W		3.26	3.26	0	SGD	635886
YPL108W YPL108W		3.02	3.02	0	SGD	634395
YPL128C TBF1,LPI16	TTAGGG repeat binding factor; lethal	0.43	-2.35	1.14E-13	SGD	639520
YPL173W MRPL40	Mitochondrial ribosomal protein MRPL40 (YmL40); ribosomal protein (YmL40)	3.27	3.27	0	SGD	634554
YPL181W YPL181W		0.31	-3.22	0	SGD	637115
YPL212C PUS1	Involved in tRNA biogenesis; tRNA pseudouridine synthase; pus1 los1 double	2.4	2.4	0	SGD	634064
YPL244C HUT1	similar to UDP-galactose transporter	2.19	2.19	0	SGD	635904
YPL246C YPL246C		2.09	2.09	4.53E-41	SGD	636547

YPL251W	YPL251W		3.62	3.62	1.16E-06	SGD	634216
YPL252C	YAH1	Yeast Adrenodoxin Homologue 1, This protein is targeted to the mitochondrial	2.19	2.19	1.45E-13	SGD	637516
YPL253C	VIK1	vegetative interaction with Kar3p; Cik1p homolog; Null mutant is viable and res	5.28	5.28	1.51E-16	SGD	637177
YPL261C	YPL261C		2.28	2.28	1.65E-27	SGD	634293
YPL268W	PLC1	Hydrolyzes phosphatidylinositol 4,5-biphosphate (PIP2) to generate two secon	0.44	-2.27	1.71E-15	SGD	637284
YPL273W	SAM4	AdoMet-homocysteine methyltransferase; Slow growth on S-adenosylmethioni	2.01	2.01	4.41E-41	SGD	635127
YPR026W	ATH1	Null mutant is viable, increased tolerance to dehydration, freezing, and toxic le	0.45	-2.24	9.27E-32	SGD	635555
YPR028W	YOP1,YIP2	Ypt Interacting Protein	0.37	-2.7	5.86E-16	SGD	634449
YPR091C	YPR091C		0.33	-3.07	3.59E-23	SGD	634819
YPR114W	YPR114W		0.4	-2.5	8.78E-12	SGD	635119
YPR117W	YPR117W		0.44	-2.26	2.80E-05	SGD	638955
YPR122W	AXL1,FUS5,STE22	determinant in axial budding pattern of haploid cells, involved in processing of ;	0.43	-2.32	3.22E-16	SGD	638867
YPR191W	QCR2,COR2,UCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2; Null mutant is viable ;	0.42	-2.38	2.05E-16	SGD	639274
YPR196W	MAL63	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain typ	0.34	-2.91	1.59E-09	SGD	636085
YPR202W	YPR202W		2.54	2.54	7.66E-07	SGD	635947

ID

BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transcription initiation from Pol III promoter|MolFunction=RNA polymerase III transcription factor|CellComponent=transcription factor TFIIIC
BioProcess=ER to Golgi transport|MolFunction=molecular_function unknown|CellComponent=COPII-coated vesicle
BioProcess=mitochondrion organization and biogenesis*|MolFunction=molecular_function unknown|CellComponent=mitochondrial outer membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=chromosome segregation|MolFunction=molecular_function unknown|CellComponent=spindle pole
BioProcess=ER-associated protein catabolism|MolFunction=molecular_function unknown|CellComponent=endoplasmic reticulum membrane, intrinsic protein
BioProcess=butanediol fermentation|MolFunction=(R,R)-butanediol dehydrogenase|CellComponent=cytoplasm
BioProcess=tRNA splicing|MolFunction=tRNA-intron endonuclease|CellComponent=nuclear inner membrane*
BioProcess=cell cycle|MolFunction=protein kinase|CellComponent=not yet annotated
BioProcess=steroid biosynthesis|MolFunction=not yet annotated|CellComponent=Golgi trans cisterna*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=acetate metabolism*|MolFunction=acetyl-CoA hydrolase|CellComponent=cytoplasm
BioProcess=proteolysis and peptidolysis*|MolFunction=ATP-dependent peptidase|CellComponent=mitochondrial matrix
BioProcess=DNA replication initiation*|MolFunction=chromatin binding*|CellComponent=cytoplasm*
BioProcess=DNA replication initiation*|MolFunction=alpha DNA polymerase|CellComponent=alpha DNA polymerase:primase complex
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=20S core proteasome
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=hydrogen-transporting ATP synthase, c
BioProcess=cell wall organization and biogenesis*|MolFunction=protein kinase C|CellComponent=cellular_component unknown
BioProcess=galactose metabolism|MolFunction=UTP-hexose-1-phosphate uridylyltransferase|CellComponent=cytoplasm
BioProcess=phosphatidylglycerol biosynthesis*|MolFunction=phosphatidate cytidylyltransferase|CellComponent=mitochondrion*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=regulation of transcription from Pol II promoter*|MolFunction=Pol I transcription termination factor|CellComponent=nucleus
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=amino acid transport|MolFunction=amino acid transporter|CellComponent=plasma membrane
BioProcess=stress response|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=vesicle-mediated transport|MolFunction=molecular_function unknown|CellComponent=cytoplasmic vesicle*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=transketolase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated

BioProcess=carbohydrate metabolism|MolFunction=D-arabinose 1-dehydrogenase [NAD(P)]|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=prephenate dehydrogenase (NADP+)|CellComponent=not yet annotated
BioProcess=rRNA processing*|MolFunction=ribonuclease P*|CellComponent=ribonuclease mitochondrial RNA processing complex*
BioProcess=cytoskeleton organization and biogenesis|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=gluconeogenesis*|MolFunction=glucose-6-phosphate isomerase|CellComponent=cytosol
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated
BioProcess=lipid transport|MolFunction=plasma membrane long-chain fatty acid transporter|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=N-linked glycosylation|MolFunction=UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosamine-1-phosphate transferase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=cell cycle|MolFunction=kinase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=mating (sensu Saccharomyces)|MolFunction=molecular_function unknown|CellComponent=plasma membrane
BioProcess=not yet annotated|MolFunction=RNA binding|CellComponent=polysome
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transport|MolFunction=ATP-binding cassette (ABC) transporter|CellComponent=cytoplasm*
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=DNA replication and chromosome cycle|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=ribokinase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=19S proteasome regulatory particle
BioProcess=intracellular accumulation of glycerol|MolFunction=glycerol-3-phosphate dehydrogenase (NAD+)|CellComponent=cytoplasm
BioProcess=pseudohyphal growth*|MolFunction=acid phosphatase|CellComponent=cellular_component unknown
BioProcess=mating (sensu Saccharomyces)|MolFunction=molecular_function unknown|CellComponent=integral membrane protein
BioProcess=protein amino acid acetylation|MolFunction=peptide alpha-N-acetyltransferase|CellComponent=not yet annotated
BioProcess=tRNA splicing|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=G2/M transition of mitotic cell cycle*|MolFunction=SUMO conjugating enzyme|CellComponent=nucleus
BioProcess=mRNA splicing|MolFunction=pre-mRNA splicing factor|CellComponent=small nuclear ribonucleoprotein complex
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=nucleotide binding|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=glutamate dehydrogenase|CellComponent=not yet annotated

BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=mating-type switching/recombination*|MolFunction=endonuclease|CellComponent=nucleus
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=integral membrane protein
BioProcess=glycogen metabolism*|MolFunction=protein phosphatase type 1|CellComponent=cytoplasm*
BioProcess=regulation of transcription from Pol II promoter*|MolFunction=DNA binding*|CellComponent=nucleus
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=tricarboxylic acid cycle*|MolFunction=succinate dehydrogenase|CellComponent=mitochondrial matrix*
BioProcess=ER to Golgi transport|MolFunction=SNARE binding|CellComponent=endoplasmic reticulum*
BioProcess=RNA splicing|MolFunction=RNA helicase|CellComponent=mitochondrial matrix
BioProcess=ubiquinone metabolism|MolFunction=not yet annotated|CellComponent=mitochondrial inner membrane
BioProcess=steroid metabolism|MolFunction=RNA polymerase II transcription factor|CellComponent=cytoplasm
BioProcess=chromatin assembly/disassembly|MolFunction=DNA binding|CellComponent=nucleosome
BioProcess=not yet annotated|MolFunction=5-aminolevulinic acid synthase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=cell cycle|MolFunction=RNA binding|CellComponent=cytoplasm
BioProcess=response to osmotic stress*|MolFunction=cytoskeletal protein binding|CellComponent=actin cortical patch (sensu Saccharomyces)
BioProcess=chromatin modification*|MolFunction=not yet annotated|CellComponent=SAGA complex
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=adenosinetriphosphatase*|CellComponent=19S proteasome regulatory particle*
BioProcess=purine nucleotide biosynthesis|MolFunction=hypoxanthine phosphoribosyltransferase|CellComponent=not yet annotated
BioProcess=sodium ion homeostasis|MolFunction=protein serine/threonine phosphatase|CellComponent=cellular_component unknown
BioProcess=polyubiquitination*|MolFunction=ubiquitin-protein ligase|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=O-linked glycosylation*|MolFunction=alpha-1,2-mannosyltransferase|CellComponent=Golgi apparatus
BioProcess=not yet annotated|MolFunction=RNA binding|CellComponent=cytoplasm*
BioProcess=mitotic spindle checkpoint|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)
BioProcess=biological_process unknown|MolFunction=adenosinetriphosphatase|CellComponent=cellular_component unknown
BioProcess=vacuolar protein catabolism*|MolFunction=endopeptidase*|CellComponent=vacuole (sensu Fungi)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=nucleus*
BioProcess=ubiquitin-dependent protein catabolism*|MolFunction=proteasome endopeptidase|CellComponent=20S core proteasome
BioProcess=not yet annotated|MolFunction=long-chain-fatty-acid-CoA-ligase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=response to oxidative stress|MolFunction=protein-methionine-S-oxide reductase|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=protein phosphatase regulator|CellComponent=protein phosphatase type 1 complex

BioProcess=hexadecanal biosynthesis|MolFunction=3-oxoacyl-[acyl-carrier protein] synthase|CellComponent=mitochondrion
BioProcess=response to osmotic stress*|MolFunction=glycerol-1-phosphatase|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=polyubiquitination*|MolFunction=ubiquitin-protein ligase|CellComponent=plasma membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=establishment of cell polarity (sensu Saccharomyces)*|MolFunction=signal transducer*|CellComponent=intracellular
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=19S proteasome regulatory particle*
BioProcess=deubiquitination|MolFunction=ubiquitin-specific protease|CellComponent=19S proteasome regulatory particle
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=20S core proteasome
BioProcess=not yet annotated|MolFunction=3-isopropylmalate dehydratase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=rRNA processing*|MolFunction=molecular_function unknown|CellComponent=nucleolus
BioProcess=regulation of transcription from Pol II promoter*|MolFunction=DNA binding*|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=35S primary transcript processing*|MolFunction=ATP dependent RNA helicase|CellComponent=nucleolus
BioProcess=poly(A)+ mRNA-nucleus export|MolFunction=poly(A) binding|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=chorismate synthase|CellComponent=not yet annotated
BioProcess=carbohydrate metabolism|MolFunction=alpha-mannosidase|CellComponent=vacuolar membrane
BioProcess=35S primary transcript processing*|MolFunction=5-3 exoribonuclease|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
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BioProcess=biological_process unknown|MolFunction=nucleotidase|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=cell wall organization and biogenesis*|MolFunction=1,3-beta-glucan synthase|CellComponent=actin cap (sensu Saccharomyces)*
BioProcess=not yet annotated|MolFunction=transaldolase|CellComponent=not yet annotated

BioProcess=mRNA processing*|MolFunction=molecular_function unknown|CellComponent=endoplasmic reticulum
BioProcess=establishment of cell polarity (sensu Saccharomyces)*|MolFunction=signal transducer*|CellComponent=intracellular
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=cell wall organization and biogenesis*|MolFunction=not yet annotated|CellComponent=integral membrane protein
BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylserine decarboxylase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=protein biosynthesis*|MolFunction=structural constituent of ribosome|CellComponent=cytosolic small ribosomal subunit (sensu Eukarya)
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial small ribosomal subunit
BioProcess=stress response|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=glycolysis|MolFunction=6-phosphofructokinase|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
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BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=protein catabolism|MolFunction=ATPase|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=alpha-glucosidase|CellComponent=not yet annotated
BioProcess=alpha-glucoside transport|MolFunction=general alpha-glucoside:hydrogen symporter*|CellComponent=membrane fraction
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=vesicle-mediated transport|MolFunction=clathrin binding|CellComponent=AP-1 adaptor complex
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=iron homeostasis*|MolFunction=siderochrome-iron transporter|CellComponent=plasma membrane
BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)
BioProcess=ergosterol biosynthesis|MolFunction=electron transporter|CellComponent=microsome
BioProcess=rRNA processing*|MolFunction=ribonuclease P*|CellComponent=ribonuclease mitochondrial RNA processing complex*
BioProcess=mRNA splicing*|MolFunction=ATP dependent RNA helicase|CellComponent=nucleolus
BioProcess=mRNA catabolism*|MolFunction=protein binding|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=hexose transport|MolFunction=glucose transporter*|CellComponent=not yet annotated
BioProcess=regulation of cell shape and cell size|MolFunction=kinase|CellComponent=cellular_component unknown
BioProcess=Golgi to vacuole transport|MolFunction=molecular_function unknown|CellComponent=Golgi trans-face
BioProcess=protein amino acid phosphorylation*|MolFunction=casein kinase I|CellComponent=endoplasmic reticulum*
BioProcess=signal transduction|MolFunction=molecular_function unknown|CellComponent=plasma membrane
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=molecular_function unknown|CellComponent=cytoplasm*
BioProcess=not yet annotated|MolFunction=threonine-tRNA ligase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown

BioProcess=tricarboxylic acid cycle*|MolFunction=oxoglutarate dehydrogenase (lipoamide)|CellComponent=mitochondrial matrix
BioProcess=carbohydrate metabolism|MolFunction=glycerol-3-phosphate dehydrogenase|CellComponent=mitochondrion
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=meiosis*|MolFunction=adenylate cyclase|CellComponent=plasma membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=nicotinamide adenine dinucleotide biosynthesis|MolFunction=arylformamidase|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=sphingolipid metabolism*|MolFunction=sphingosine-1-phosphate phosphatase|CellComponent=endoplasmic reticulum
BioProcess=protein amino acid glycosylation|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylethanolamine N-methyltransferase|CellComponent=endoplasmic reticulum
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=hydrogen-transporting ATP synthase, c
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cell wall (sensu Fungi)
BioProcess=aldehyde metabolism|MolFunction=benzyl alcohol dehydrogenase|CellComponent=cellular_component unknown
BioProcess=polyubiquitination*|MolFunction=ubiquitin-protein ligase|CellComponent=cellular_component unknown
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=transcription|MolFunction=transcription factor|CellComponent=not yet annotated
BioProcess=glucose metabolism|MolFunction=DNA binding*|CellComponent=not yet annotated
BioProcess=ubiquitin-dependent protein catabolism*|MolFunction=molecular_function unknown|CellComponent=nucleus
BioProcess=respiratory gaseous exchange|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=gluconeogenesis*|MolFunction=fructose-bisphosphate aldolase|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=aspartate catabolism|MolFunction=aspartate aminotransferase|CellComponent=mitochondrion

BioProcess=not yet annotated|MolFunction=DNA-(apurinic or apyrimidinic site) lyase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=MAPKKK cascade|MolFunction=receptor signaling protein serine/threonine kinase|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=tRNA splicing|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=iron homeostasis|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=G1/S transition of mitotic cell cycle|MolFunction=protein serine/threonine phosphatase|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=bilirubin transport|MolFunction=bilirubin transporter|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=Golgi retention|MolFunction=molecular_function unknown|CellComponent=extrinsic membrane protein
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=cytochrome c oxidase|CellComponent=respiratory chain complex IV (sensu Eukarya)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=signal peptide processing|MolFunction=signal peptidase|CellComponent=signal peptidase complex
BioProcess=protein biosynthesis*|MolFunction=translation regulator|CellComponent=mitochondrial inner membrane*
BioProcess=protein biosynthesis*|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=cell wall (sensu Fungi)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=lipid binding*|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=methionine metabolism|MolFunction=methionine adenosyltransferase|CellComponent=cytoplasm
BioProcess=sterol metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=microtubule nucleation*|MolFunction=structural constituent of cytoskeleton|CellComponent=inner plaque of spindle pole body*
BioProcess=iron homeostasis|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=1-phosphatidylinositol 4-kinase|CellComponent=plasma membrane
BioProcess=dicarboxylic acid transport|MolFunction=dicarboxylic acid transporter|CellComponent=mitochondrial membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

BioProcess=establishment of cell polarity (sensu Saccharomyces)*|MolFunction=signal transducer*|CellComponent=bud tip
BioProcess=fatty acid biosynthesis*|MolFunction=molecular_function unknown|CellComponent=endoplasmic reticulum membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=signal transduction*|MolFunction=GTPase activator|CellComponent=plasma membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=double-strand break repair via homologous recombination*|MolFunction=DNA repair protein|CellComponent=nucleus
BioProcess=not yet annotated|MolFunction=AMP deaminase|CellComponent=not yet annotated
BioProcess=transcription from Pol I promoter|MolFunction=RNA polymerase I transcription factor|CellComponent=RNA polymerase I transcription factor complex
BioProcess=mRNA splicing|MolFunction=not yet annotated|CellComponent=snRNP U1*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=20S core proteasome
BioProcess=processing of 20S pre-rRNA|MolFunction=snoRNA binding|CellComponent=small nucleolar ribonucleoprotein complex
BioProcess=stress response*|MolFunction=alpha,alpha-trehalose-phosphate synthase (UDP-forming)|CellComponent=alpha, alpha-trehalose-phosphate synthase cc
BioProcess=DNA repair*|MolFunction=molecular_function unknown|CellComponent=chromatin assembly complex
BioProcess=ubiquinone metabolism|MolFunction=not yet annotated|CellComponent=mitochondrion
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=protein-vacuolar targeting|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=pantothenate biosynthesis|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=acylglycerone-phosphate reductase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=mRNA-nucleus export*|MolFunction=structural molecule|CellComponent=nuclear pore*
BioProcess=ethanol fermentation|MolFunction=NADH dehydrogenase|CellComponent=mitochondrion
BioProcess=mRNA-nucleus export*|MolFunction=structural molecule|CellComponent=nuclear pore
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=stress response|MolFunction=aldehyde dehydrogenase|CellComponent=cytoplasm
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=ER to Golgi transport|MolFunction=molecular_function unknown|CellComponent=TRAPP
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=nuclear fusion during karyogamy*|MolFunction=molecular_function unknown|CellComponent=shmoo tip
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=cytochrome c oxidase|CellComponent=respiratory chain complex IV (sensu Eukarya)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=spindle pole body duplication (sensu Saccharomyces)|MolFunction=protein degradation tagging|CellComponent=nucleus
BioProcess=gluconeogenesis|MolFunction=transcription factor|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=carboxypeptidase C|CellComponent=cytoplasm*
BioProcess=deubiquitination|MolFunction=ubiquitin-specific protease|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=vacuole fusion (non-autophagic)*|MolFunction=endopeptidase inhibitor|CellComponent=cytoplasm*
BioProcess=protein amino acid phosphorylation*|MolFunction=protein serine/threonine kinase|CellComponent=actin cortical patch (sensu Saccharomyces)
BioProcess=chromatin assembly/disassembly|MolFunction=DNA binding|CellComponent=nucleosome
BioProcess=cell cycle|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=cytoplasm
BioProcess=tricarboxylic acid cycle*|MolFunction=isocitrate dehydrogenase (NAD+)|CellComponent=mitochondrial matrix
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=lysine-tRNA ligase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=chromatin modification|MolFunction=molecular_function unknown|CellComponent=nucleus
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=cytoskeleton organization and biogenesis*|MolFunction=cytoskeletal protein binding*|CellComponent=actin cortical patch (sensu Saccharomyces)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transcription from Pol III promoter|MolFunction=DNA-directed RNA polymerase III|CellComponent=DNA-directed RNA polymerase III complex
BioProcess=ribosome biogenesis|MolFunction=translation elongation factor|CellComponent=cytoplasm
BioProcess=regulation of nitrogen utilization|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=spindle pole body duplication (sensu Saccharomyces)*|MolFunction=structural molecule|CellComponent=half bridge of spindle pole body
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=DNA replication|MolFunction=ATPase*|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=basic amino acid transport|MolFunction=basic amino acid transporter|CellComponent=plasma membrane
BioProcess=ergosterol biosynthesis|MolFunction=C-14 sterol reductase|CellComponent=endoplasmic reticulum

BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=mRNA polyadenylation*|MolFunction=cleavage/polyadenylation specificity factor|CellComponent=mRNA cleavage and polyadenylation specificity factor
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=peroxisome organization and biogenesis|MolFunction=adenosinetriphosphatase|CellComponent=peroxisome
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=sterol metabolism|MolFunction=sterol O-acyltransferase|CellComponent=endoplasmic reticulum
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=hexose transport|MolFunction=glucose transporter*|CellComponent=not yet annotated
BioProcess=ER-associated protein catabolism|MolFunction=ubiquitin-protein ligase|CellComponent=endoplasmic reticulum membrane
BioProcess=protein amino acid phosphorylation*|MolFunction=calcium/calmodulin-dependent protein kinase|CellComponent=cytoplasm
BioProcess=aromatic amino acid transport|MolFunction=aromatic amino acid transporter|CellComponent=plasma membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transcriptional gene silencing|MolFunction=NAD-dependent histone deacetylase*|CellComponent=histone deacetylase complex
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=acylglycerone-phosphate reductase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transcription initiation from Pol II promoter*|MolFunction=specific RNA polymerase II transcription factor|CellComponent=nucleus
BioProcess=mismatch repair*|MolFunction=adenosinetriphosphatase*|CellComponent=DNA replication factor C complex
BioProcess=ubiquinone metabolism|MolFunction=hexaprenyldihydroxybenzoate methyltransferase|CellComponent=not yet annotated
BioProcess=synapsis|MolFunction=molecular_function unknown|CellComponent=telomere
BioProcess=manganese ion transport|MolFunction=manganese ion transporter|CellComponent=plasma membrane*
BioProcess=di-, tri-valent inorganic cation transport|MolFunction=di-, tri-valent inorganic cation transporter|CellComponent=plasma membrane
BioProcess=ubiquitin-dependent protein catabolism*|MolFunction=protein binding*|CellComponent=nuclear ubiquitin ligase complex
BioProcess=protein biosynthesis|MolFunction=protein phosphatase type 2A|CellComponent=cytoplasm*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=heavy metal sensitivity/resistance|MolFunction=copper binding|CellComponent=cytoplasm
BioProcess=carbohydrate metabolism|MolFunction=hydroxyacylglutathione hydrolase|CellComponent=mitochondrion*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=complex III (ubiquinone to cytochrome c)*|MolFunction=electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex|CellC
BioProcess=vesicle-mediated transport|MolFunction=RAB GTPase activator|CellComponent=Golgi apparatus

BioProcess=cell wall organization and biogenesis*|MolFunction=inositol-1,4,5-trisphosphate 5-phosphatase|CellComponent=membrane fraction
BioProcess=tricarboxylic acid cycle*|MolFunction=isocitrate dehydrogenase (NAD+)|CellComponent=mitochondrion*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=meiosis*|MolFunction=protein phosphatase type 1|CellComponent=protein phosphatase type 1 complex
BioProcess=RNA processing|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=inner mitochondrial membrane organization and biogenesis|MolFunction=molecular_function unknown|CellComponent=mitochondrial inner membrane
BioProcess=polyamine transport|MolFunction=spermine transporter|CellComponent=vacuolar membrane
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=protein folding*|MolFunction=protein disulfide isomerase|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=arginine biosynthesis|MolFunction=carbamoyl-phosphate synthase (glutamine-hydrolyzing)|CellComponent=cytosol
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=rRNA modification*|MolFunction=snoRNA binding|CellComponent=small nuclear ribonucleoprotein complex*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=protein secretion|MolFunction=molecular_function unknown|CellComponent=peripheral membrane protein of membrane fraction
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=translational initiation|MolFunction=translation initiation factor|CellComponent=cytoplasm*
BioProcess=signal transduction|MolFunction=signal transducer|CellComponent=cellular_component unknown
BioProcess=not yet annotated|MolFunction=alcohol O-acetyltransferase|CellComponent=not yet annotated
BioProcess=nucleotide-excision repair, DNA incision, 5 to lesion|MolFunction=single-stranded DNA specific endodeoxyribonuclease|CellComponent=nucleotide excision repair
BioProcess=not yet annotated|MolFunction=protein kinase|CellComponent=not yet annotated
BioProcess=invasive growth|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=mannose-inositol-P-ceramide (MIPC) metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=signal transduction|MolFunction=molecular_function unknown|CellComponent=cellular_component unknown
BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=nucleus
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=not yet annotated|MolFunction=pseudouridylate synthase|CellComponent=not yet annotated
BioProcess=UDP-galactose transport|MolFunction=UDP-galactose transporter|CellComponent=cellular_component unknown
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated

BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=heme a biosynthesis|MolFunction=Fe2S2 electron transfer carrier|CellComponent=mitochondrial matrix
BioProcess=microtubule-based process|MolFunction=microtubule motor|CellComponent=spindle pole body*
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=pseudohyphal growth*|MolFunction=1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase|CellComponent=cellular_component unknown
BioProcess=sulfur amino acid metabolism|MolFunction=homocysteine S-methyltransferase|CellComponent=cellular_component unknown
BioProcess=stress response*|MolFunction=alpha,alpha-trehalase|CellComponent=vacuole (sensu Fungi)
BioProcess=biological_process unknown|MolFunction=molecular_function unknown|CellComponent=not yet annotated
BioProcess=mating (sensu Saccharomyces)*|MolFunction=metalloendopeptidase|CellComponent=intracellular
BioProcess=aerobic respiration*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=mitochondrion*

atalytic core (sensu Eukarya)

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catalytic core (sensu Eukarya)

complex (UDP-forming)

comple;

Component=mitochondrial inner membrane*

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